J. Andres

1646

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/029,042B

DATE: 11/13/2000
TIME: 12:44:10

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11132000\I029042B.raw

```
 4 <110> APPLICANT: Kim, Sun-Young
 5         Kim, Kee-Won
 6         Kim, Tae-Han
 7         Hwang, Jeong-Ho
 8         Kim, Seon-Hee
 9         Lee, Sun-Young
11 <120> TITLE OF INVENTION: Heterologous Protein Production System using Avian Cells
 0 <130> FILE REFERENCE:
13 <140> CURRENT APPLICATION NUMBER: US 09/029,042B
15 <141> CURRENT FILING DATE: 1998-05-15
17 <150> PRIOR APPLICATION NUMBER: PCT/KR96/00145
19 <151> PRIOR FILING DATE: 1996-08-23
21 <160> NUMBER OF SEQ ID NOS: 11
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ERRORED SEQUENCES

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 68 <210> SEQ ID NO: 2        1533 (next page)
 70 <211> LENGTH: 1583
 72 <212> TYPE: DNA
 74 <213> ORGANISM: erythropoietin
 76 <400> SEQUENCE: 2
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 85    ctacgcctgt ggccagggcc agagccttca gggacccttg actccccggg 400
 86    ctgtgtgcat ttcagacggg ctgtgctgaa cactgcagct tgaatgagaa 450
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 88    aggtgagttc cttttttttt ttttttcctt tcttttggag aatctcattt 550
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102    ccttcgcagc ctcaccactc tgcttcgggc tctgggagcc caggtgagta 1250
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11/13/00

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11132000\I029042B.raw

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106    tgcggcctca gctgctccac tccgaacaat cactgctgac actttccgca 1450
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253 <213> ORGANISM: erythropoietin
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411 <212> TYPE: PRT
413 <213> ORGANISM: erythropoietin gene
415 <400> SEQUENCE: 10
417    Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
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[handwritten annotation:] 1583 1533

[handwritten annotation:] "i" is invalid for use in the sequence, per Sequence Rules. Use "n" and explain in ∠2207-∠2237 section.

[handwritten annotation:] next page

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/029,042B

DATE: 11/13/2000
TIME: 12:44:10

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11132000\I029042B.raw

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  420                         20                      25                       30
  421     Ile Cys Asp Arg Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
  422                 35                      40                       45
  423     Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
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  425     Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
  426     65                      70                      75                       80
  427     Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
  428                     85                      90                       95
  429     Leu Ser Glu Ser Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
                        100          100           105    105          110     110
E-->  430     Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
  431                 115                     120                      125
E-->  432     Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
  433             130                     135                      140
E-->  434     Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
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E-->  436     Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
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  458                         20                      25                       30
  459     Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
  460                 35                      40                       45
  461     Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
  462             50                      55                       60
  463     Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
  464     65                      70                      75                       80
  465     Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
  466                     85                      90                       95
  467     Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
  468                 100                     105                      110
  469     Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
  470                 115                     120                      125
  471     Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
  472             130                     135                      140
  473     Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
  474     145                     150                     155                      160
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next page

*misaligned
amino acid numbers

see item 4
in Exam Summary
Sheet*

```
475    Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
476                     165             170                 175
477    Arg Gly Glu Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
478                 180             185                 190
479    Gly
E--> 480 1
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delete at end of file

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/029,042B

DATE: 11/13/2000
TIME: 12:44:11

Input Set : **A:\PTO.txt**
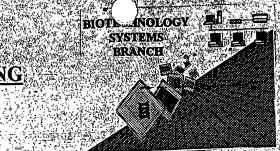Output Set: **N:\CRF3\11132000\I029042B.raw**

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:1583 Counted:1533 SEQ:2
L:108 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1583 Found:1533 SEQ:2
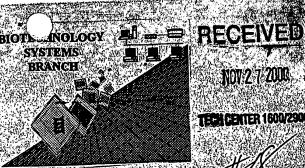L:278 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:430 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:480 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11

file://C:\Crf3\Outhold\VsrI029042B.htm

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/029,042B_

Source: _1646_

Date Processed by STIC: _11/13/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY** or,
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: _09/029,042B_

RECEIVED

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

TECH CENTER 1600/2900

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid-number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 __╪___ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 __✓___ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.